2. **Tyrosine phosphatases** dephosphorylate tyrosine (Tyr) residues in proteins and share a conserved active-site sequence motif Cys-X5-Arg (X = any amino acid residue) [SEQ ID NO:1] and a Asp located in a surface loop. Protein tyrosine phosphatases (PTPs) are characterized by a signature sequence motif of 11 amino acid residues, (Ile/Val)-His-Cys-X-Ala-Gly-X-Gly-Arg-(Ser/Thr)-Gly [SEQ ID NO:2] that is found in most PTPs. The diversity within the PTPs arises from the variable N- or C-terminal sequences attached to the core catalytic domain.

Page 37, please delete the second full paragraph, and replace it with the following new paragraph:

3. **Dual-specificity phosphatases** dephosphorylate Ser/Thr residues in addition to Tyr residues in proteins. Their signature motif, His-Cys-X-X-Gly-X-X-Arg-(Ser/Thr) [SEQ ID NO:3] is analogous to PTPs but these phosphatases display a restricted substrate specificity.

Page 59, please delete the first full paragraph, and replace it with the following new paragraph:

Total RNA was isolated from control (5.5mM glucose) or glucose-treated (25mM glucose) A10 cells and 2 μg was used to synthesize first strand cDNA using an Oligo(dT) primer and Superscript II reverse transcriptase (Life Technologies Pre-amplification Kit). The upstream sense primer corresponded to the C4 kinase domain common to both PKCβI and PKCβII (5' CGTATATGCGGCCGCGTTGTGGGCCTGAAGGGG 3') [SEQ ID NO:4] and the downstream antisense primer was specific for PKCβI (5' GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 3') [SEQ ID NO:5] (Chalfont *et al.*,

1995, pp.13326-13332.). These primers detect inclusion of the PKCβII exon in the mature mRNA as well as PKCβI mRNA. Sense and antisense primers for β-actin (#5402-3) were obtained from Clonetech. PCR was performed using ampliTaq Gold DNA polymerase from Perkin Elmer (#N808-0240) on 10% of the reverse transcriptase reaction product. Following 35 cycles of amplification in a Biometra Trioblock thermocycler (PKCβI and –βII: 95°C, 30 sec; 64 °C, 2min for 35 cycles; and for β-actin: 94 °C, 1 min; 58 °C, 1 min; and 72 °C, 3 min for 35 cycles), 25% of the PCR reaction was resolved on a 1.2% agarose gel. Bands were observed under UV light and photographed.

Page 60, please delete the first full paragraph, and replace it with the following new paragraph:

For the stability reporter system, β-globin primers were designed. The sense primer was (5' GCATCTGTCCAGTGAGGAGAA 3') [SEQ ID NO:6] while the antisense primer for β-globin was (5' AACCAGCACGTTGCCCAGGAG 3') [SEQ ID NO:7]. PCR was performed using ampliTaq Gold DNA polymerase from Perkin Elmer (#N808-0240) on 10% of the reverse transcriptase reaction product. Following 25 cycles of amplification in a Biometra Trioblock thermocycler (94°C, 1 min; 58 °C, 1 min; and 72 °C, 3 min for 25 cycles), 25% of the PCR reaction was resolved on a 1.2% agarose gel. Bands were observed under UV light and photographed. The expected size of the amplified product was 320 bp.

Page 62, please delete the first full paragraph, and replace it with the following new paragraph:

The 404bp PKCβII product was obtained by PCR amplification using sense primer to the upstream PKCβ common C4 domain (5' CGTATATGCGGCCGCGTTGTGGGCCTGAAGGGG 3') [SEQ ID NO:8] and anti-sense primer to βIV5 domain (5' GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 3') [SEQ ID NO:9] such that the exon-included PKCβII mRNA was amplified. This PKCβII cDNA piece was cloned into the pCR-Blunt vector (Invitrogen) such that the sense transcripts could be generated from the upstream T7 RNA polymerase promoter. A 410 bp β-globin segment cloned into the pCR-Blunt vector was used as a non-specific competitor probe.

Page 84, please delete the fourth full paragraph, and replace it with the following new paragraph:

5'TTTTAAACCAAAAGCTTTTTGGGCGAAACGCTGAAACTTCGACCGGTTTTTCACCC
GCCATCCACCAGTCCTAACACCTCCGACCAGGAAGTCATCAGGAATATTGACCAATC
AGAATTCGAAGGATTTCCTTTGTTAACTCTGAATTTTTAAAACCCGAAGTCAAGAGC
TAGTAGATCTGTAGACCTCCGTCCTTCATTTCTGTCATTCAAGCTCACAGCTATCATG
AGAGACAAGCGAGACACCTCTCCCACTGACAAACTCTGTCGACTAGAATGCCCTGA
ATTCTGCAGATATCCATCACACTGCG 3'

Page 84, please delete the fifth full paragraph, and replace it with the following new paragraph:

Figure 27. PKC βII cDNA (350 bp) sequence [SEQ ID NO:10]

Page 125, please delete the second full paragraph, and replace it with the following new paragraph:

B9

UUUUAAACCA AAAGCUUUUU GGGCGAAACG CUGAAACUUC GACCGGUUUU
UCACCCGCCA UCCACCAGUC CUAACACCUC CGACCAGGAA GUCAUCAGGA
AUAUUGACCA AUCAGAAUUC GAAGGAUUUC CUUUGUUAAC UCUGAAUUUU
UAAAACCCGA AGUCAAGAGC UAGUAGAUCU GUAGACCUCC GUCCUUCAUU
UCUGUCAUUC AAGCUCACAG CUAUCAUGAG AGACAAGCGA GACACCUCCA
ACUUCGACAA AAGUUCACCA GGCAGCCUGU GGAACUGACU CCCACUGACA

NE **Page 126, please delete the first full paragraph, and replace it with the following new paragraph:**

B10

Figure 43. PKCβII mRNA sequence [SEQ ID NO:13] linearized at 175 bp with *Bgl II* and RNA secondary structure analysis.

NE **Page 126, please delete the second full paragraph, and replace it with the following new paragraph:**

B11

UUUUAAACCA AAAGCUUUUU GGGCGAAACG CUGAAACUUC GACCGGUUUU
UCACCCGCCA UCCACCAGUC CUAACACCUC CGACCAGGAA GUCAUCAGGA
AUAUUGACCA AUCAGAAUUC GAAGGAUUUC CUUUGUUAAC UCUGAAUUUU
UAAAACCCGA AGUCAAGAGC UAGUA

NE **Page 127, please delete the first full paragraph, and replace it with the following new paragraph:**

B12

Figure 44. PKCβII mRNA sequence [SEQ ID NO:14] linearized at 137 bp with *Hpa I* and RNA secondary structure analysis.

NE **Page 127, please delete the first full paragraph, and replace it with the following new paragraph:**